



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/803,459A
Source: FWO
Date Processed by STIC: 7/29/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04): U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/803,459A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.

4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213>
Response Per 1.823 of Sequence Rules, the **only valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
34,6

11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/803,459A

DATE: 07/29/2004
TIME: 09:36:52

Input Set : D:\Leptin Sequence Listing-Corrected.txt
Output Set: N:\CRF4\07292004\J803459A.raw

3 <110> APPLICANT: Gertler, Arieh
4 Krishna, Radha G.
6 <120> TITLE OF INVENTION: LEPTIN BINDING DOMAIN COMPOSITIONS AND METHODS THERETO
8 <130> FILE REFERENCE: 28758.1
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/803,459A
C--> 10 <141> CURRENT FILING DATE: 2004-03-19
10 <160> NUMBER OF SEQ ID NOS: 8
12 <170> SOFTWARE: PatentIn version 3.2
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 630
16 <212> TYPE: DNA
17 <213> ORGANISM: homo sapiens
20 <220> FEATURE:
21 <221> NAME/KEY: CDS
22 <222> LOCATION: (1)..(630)
24 <220> FEATURE:
25 <221> NAME/KEY: misc_feature
26 <222> LOCATION: (6)..(6)
27 <223> OTHER INFORMATION: n is a, c, g, or t
29 <400> SEQUENCE: 1

W--> 30 atg gcn att gat gtc aat atc aat atc tca tgt gaa act gat ggg tac 48
31 Met Ala Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr Asp Gly Tyr
32 1 5 10 15
34 tta act aaa atg act tgc aga tgg tca acc agt aca atc cag tca ctt 96
35 Leu Thr Lys Met Thr Cys Arg Trp Ser Thr Ser Thr Ile Gln Ser Leu
36 20 25 30
38 gcg gaa agc act ttg caa ttg agg tat cat agg agc agc ctt tac tgt 144
39 Ala Glu Ser Thr Leu Gln Leu Arg Tyr His Arg Ser Ser Leu Tyr Cys
40 35 40 45
42 tct gat att cca tct att cat ccc ata tct gag ccc aaa gat tgc tat 192
43 Ser Asp Ile Pro Ser Ile His Pro Ile Ser Glu Pro Lys Asp Cys Tyr
44 50 55 60
46 ttg cag agt gat ggt ttt tat gaa tgc att ttc cag cca atc ttc cta 240
47 Leu Gln Ser Asp Gly Phe Tyr Glu Cys Ile Phe Gln Pro Ile Phe Leu
48 65 70 75 80
50 tta tct ggc tac aca atg tgg att agg atc aat cac tct cta ggt tca 288
51 Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser Leu Gly Ser
52 85 90 95
54 ctt gac tct cca cca aca tgt gtc ctt cct gat tct gtg gtg aag cca 336
55 Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val Val Lys Pro
56 100 105 110
58 ctg cct cca tcc agt gtg aaa gca gaa att act ata aac att gga tta 384
59 Leu Pro Pro Ser Ser Val Lys Ala Glu Ile Thr Ile Asn Ile Gly Leu

P.3
Does Not Comply
Corrected Diskette Needed

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Input Set : D:\Leptin Sequence Listing-Corrected.txt
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60	115	120	125	
62	ttg aaa ata tct tgg gaa aag cca gtc ttt cca gag aat aac ctt caa			432
63	Leu Lys Ile Ser Trp Glu Lys Pro Val Phe Pro Glu Asn Asn Leu Gln			
64	130	135	140	
66	ttc cag att cgc tat ggt tta agt gga aaa gaa gta caa tgg aag atg			480
67	Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Val Gln Trp Lys Met			
68	145	150	155	160
70	tat gag gtt tat gat gca aaa tca aaa tct gtc agt ctc cca gtt cca			528
71	Tyr Glu Val Tyr Asp Ala Lys Ser Lys Ser Val Ser Leu Pro Val Pro			
72	165	170	175	
74	gac ttg tgt gca gtc tat gct gtt cag gtg cgc tgt aag agg cta gat			576
75	Asp Leu Cys Ala Val Tyr Ala Val Gln Val Arg Cys Lys Arg Leu Asp			
76	180	185	190	
78	gga ctg gga tat tgg agt aat tgg agc aat cca gcc tac aca gtt gtc			624
79	Gly Leu Gly Tyr Trp Ser Asn Trp Ser Asn Pro Ala Tyr Thr Val Val			
80	195	200	205	
82	atg gat			630
83	Met Asp			
84	210			
87	<210> SEQ ID NO: 2			
88	<211> LENGTH: 210			
89	<212> TYPE: PRT			
90	<213> ORGANISM: homo sapiens			
92	<400> SEQUENCE: 2			
94	Met Ala Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr Asp Gly Tyr			
95	1	5	10	15
98	Leu Thr Lys Met Thr Cys Arg Trp Ser Thr Ser Thr Ile Gln Ser Leu			
99	20	25	30	
102	Ala Glu Ser Thr Leu Gln Leu Arg Tyr His Arg Ser Ser Leu Tyr Cys			
103	35	40	45	
106	Ser Asp Ile Pro Ser Ile His Pro Ile Ser Glu Pro Lys Asp Cys Tyr			
107	50	55	60	
110	Leu Gln Ser Asp Gly Phe Tyr Glu Cys Ile Phe Gln Pro Ile Phe Leu			
111	65	70	75	80
114	Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser Leu Gly Ser			
115	85	90	95	
118	Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val Val Lys Pro			
119	100	105	110	
122	Leu Pro Pro Ser Ser Val Lys Ala Glu Ile Thr Ile Asn Ile Gly Leu			
123	115	120	125	
126	Leu Lys Ile Ser Trp Glu Lys Pro Val Phe Pro Glu Asn Asn Leu Gln			
127	130	135	140	
130	Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Val Gln Trp Lys Met			
131	145	150	155	160
134	Tyr Glu Val Tyr Asp Ala Lys Ser Lys Ser Val Ser Leu Pro Val Pro			
135	165	170	175	
138	Asp Leu Cys Ala Val Tyr Ala Val Gln Val Arg Cys Lys Arg Leu Asp			
139	180	185	190	
142	Gly Leu Gly Tyr Trp Ser Asn Trp Ser Asn Pro Ala Tyr Thr Val Val			

RAW SEQUENCE LISTING
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Input Set : D:\Leptin Sequence Listing-Corrected.txt
Output Set: N:\CRF4\07292004\J803459A.raw

143 195 200 205

146 Met Asp
147 210

150 <210> SEQ ID NO: 3
151 <211> LENGTH: 36

152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence

155 <220> FEATURE:

W--> 156 <221> NAME/KEY:

157 <222> LOCATION:

158 <223> OTHER INFORMATION:

W--> 160 <400> 3

161 ggaattccat atgattgtatg tcaatatcaa tatctc

164 <210> SEQ ID NO: 4

165 <211> LENGTH: 39

166 <212> TYPE: DNA

167 <213> ORGANISM: Artificial Sequence

169 <220> FEATURE:

W--> 170 <221> NAME/KEY:

171 <222> LOCATION:

172 <223> OTHER INFORMATION:

W--> 174 <400> 4

175 cataggaagc tttcaatcca tgacaactgt gtaggctgg

178 <210> SEQ ID NO: 5

179 <211> LENGTH: 12

180 <212> TYPE: PRT

181 <213> ORGANISM: homo sapiens

184 <220> FEATURE:

185 <221> NAME/KEY: misc_feature

186 <222> LOCATION: (11)..(11)

187 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

189 <400> SEQUENCE: 5

36

39

needs explanation in <2207-2237 section.
(see item 11 on Error summary sheet.)

same error

W--> 191 Met Ala Ile Asp Val Asn Ile Asn Ile Ser Xaa Glu

192 1 5 10

195 <210> SEQ ID NO: 6

196 <211> LENGTH: 5

197 <212> TYPE: PRT

198 <213> ORGANISM: Artificial Sequence

201 <220> FEATURE:

202 <221> NAME/KEY: misc_feature

203 <222> LOCATION: (3)..(3)

204 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

206 <400> SEQUENCE: 6

needs explanation in <2207-2237 section

W--> 208 Trp Ser Xaa Trp Ser

209 1 5

212 <210> SEQ ID NO: 7

213 <211> LENGTH: 627

214 <212> TYPE: DNA

215 <213> ORGANISM: gallus domesticus

RAW SEQUENCE LISTING

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Input Set : D:\Leptin Sequence Listing-Corrected.txt
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218 <220> FEATURE:
 219 <221> NAME/KEY: CDS
 220 <222> LOCATION: (1)..(627)
 222 <220> FEATURE:
 223 <221> NAME/KEY: misc_feature
 224 <222> LOCATION: (6)..(6)
 225 <223> OTHER INFORMATION: n is a, c, g, or t
 227 <400> SEQUENCE: 7

W--> 228 atg gcn gta gat gtg aat atc aat atc aaa tgt gaa act gat ggg tac 48
 229 Met Ala Val Asp Val Asn Ile Asn Ile Lys Cys Glu Thr Asp Gly Tyr
 230 1 5 10 15
 232 tta act aaa atg act tgc aga tgg tct gca aac cca aac gca ttg ctc 96
 233 Leu Thr Lys Met Thr Cys Arg Trp Ser Ala Asn Pro Asn Ala Leu Leu
 234 20 25 30
 236 ttg ggg agt tcc ttg cag tta aga tac cac agg agc aaa att tat tgt 144
 237 Leu Gly Ser Ser Leu Gln Leu Arg Tyr His Arg Ser Lys Ile Tyr Cys
 238 35 40 45
 240 tct aac ttt cca agt act cct cca gaa tca gag gtg aaa gaa tgc cat 192
 241 Ser Asn Phe Pro Ser Thr Pro Pro Glu Ser Glu Val Lys Glu Cys His
 242 50 55 60
 244 ttc cag agg aat cat tct tat gag tgc aca ttt cag cct gtt ttt ctt 240
 245 Phe Gln Arg Asn His Ser Tyr Glu Cys Thr Phe Gln Pro Val Phe Leu
 246 65 70 75 80
 248 tta tct gga tat acc atg tgg att gag ctt aag cac tcg ctg gga aca 288
 249 Leu Ser Gly Tyr Thr Met Trp Ile Glu Leu Lys His Ser Leu Gly Thr
 250 85 90 95
 252 ctt gaa tcc tca cca act tgt gtc gtt cca gca gat gtg gtg aag cca 336
 253 Leu Glu Ser Ser Pro Thr Cys Val Val Pro Ala Asp Val Val Lys Pro
 254 100 105 110
 256 ctg cct ccc tcc aac att aaa gca gag atc acc aga aac gat ggg ctg 384
 257 Leu Pro Pro Ser Asn Ile Lys Ala Glu Ile Thr Arg Asn Asp Gly Leu
 258 115 120 125
 260 ctg aac gtg agc tgg aca aac ccc gtg ttt aca aat gat gac ctt aag 432
 261 Leu Asn Val Ser Trp Thr Asn Pro Val Phe Thr Asn Asp Asp Leu Lys
 262 130 135 140
 264 ttt cag atc cgg tac gca gtg aac agg gaa gaa ctc aca tgg gag ctg 480
 265 Phe Gln Ile Arg Tyr Ala Val Asn Arg Glu Glu Leu Thr Trp Glu Leu
 266 145 150 155 160
 268 tat gaa gtt cta agc gta cca aca aga tca gct gtg ata gaa gtg caa 528
 269 Tyr Glu Val Leu Ser Val Pro Thr Arg Ser Ala Val Ile Glu Val Gln
 270 165 170 175
 272 ctt tgt gtt gaa tat att gtt cag atc cgc tgc aga gcc ctg gat ggc 576
 273 Leu Cys Val Glu Tyr Ile Val Gln Ile Arg Cys Arg Ala Leu Asp Gly
 274 180 185 190
 276 tta ggc tac tgg agc aac tgg agc aga tca gcc tat gca gct gta aaa 624
 277 Leu Gly Tyr Trp Ser Asn Trp Ser Arg Ser Ala Tyr Ala Ala Val Lys
 278 195 200 205
 280 gat 627
 281 Asp

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Input Set : D:\Leptin Sequence Listing-Corrected.txt
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285 <210> SEQ ID NO: 8
286 <211> LENGTH: 209
287 <212> TYPE: PRT
288 <213> ORGANISM: gallus domesticus
290 <400> SEQUENCE: 8
292 Met Ala Val Asp Val Asn Ile Asn Ile Lys Cys Glu Thr Asp Gly Tyr
293 1 5 10 15
296 Leu Thr Lys Met Thr Cys Arg Trp Ser Ala Asn Pro Asn Ala Leu Leu
297 20 25 30
300 Leu Gly Ser Ser Leu Gln Leu Arg Tyr His Arg Ser Lys Ile Tyr Cys
301 35 40 45
304 Ser Asn Phe Pro Ser Thr Pro Pro Glu Ser Glu Val Lys Glu Cys His
305 50 55 60
308 Phe Gln Arg Asn His Ser Tyr Glu Cys Thr Phe Gln Pro Val Phe Leu
309 65 70 75 80
312 Leu Ser Gly Tyr Thr Met Trp Ile Glu Leu Lys His Ser Leu Gly Thr
313 85 90 95
316 Leu Glu Ser Ser Pro Thr Cys Val Val Pro Ala Asp Val Val Lys Pro
317 100 105 110
320 Leu Pro Pro Ser Asn Ile Lys Ala Glu Ile Thr Arg Asn Asp Gly Leu
321 115 120 125
324 Leu Asn Val Ser Trp Thr Asn Pro Val Phe Thr Asn Asp Asp Leu Lys
325 130 135 140
328 Phe Gln Ile Arg Tyr Ala Val Asn Arg Glu Glu Leu Thr Trp Glu Leu
329 145 150 155 160
332 Tyr Glu Val Leu Ser Val Pro Thr Arg Ser Ala Val Ile Glu Val Gln
333 165 170 175
336 Leu Cys Val Glu Tyr Ile Val Gln Ile Arg Cys Arg Ala Leu Asp Gly
337 180 185 190
340 Leu Gly Tyr Trp Ser Asn Trp Ser Arg Ser Ala Tyr Ala Ala Val Lys
341 195 200 205
344 Asp

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/29/2004
PATENT APPLICATION: US/10/803,459A TIME: 09:36:53

Input Set : D:\Leptin Sequence Listing-Corrected.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 6

Seq#:5; Xaa Pos. 11

Seq#:6; Xaa Pos. 3

Seq#:7; N Pos. 6

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/803,459A

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Input Set : D:\Leptin Sequence Listing-Corrected.txt
Output Set: N:\CRF4\07292004\J803459A.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:30 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:156 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:160 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:158
L:170 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:174 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:172
L:191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0